

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 20:54:52 ; Search time 1417.73 Seconds
(without alignments)
453.817 Million cell updates/sec

Title: US-09-432-546-15

Sequence: 1 agagatgacctgtgtgaccttggaatgaccttatt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:.*
1: gb_ba:.*
2: gb_hlg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pac:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_om:.*
20: em_or:.*
21: em_ov:.*
22: em_pat:.*
23: em_ph:.*
24: em_pl:.*
25: em_ro:.*
26: em_sts:.*
27: em_sy:.*
28: em_un:.*
29: em_vl:.*
30: em_hlg_hum:.*
31: em_hlg_in:.*
32: em_hlg_hum:.*
33: em_hlg_hum:.*
34: em_hlg_in:.*
35: em_hlg_rod:.*
36: em_hlg_other:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24.6	63.1	178904	2	AL354989 Homo sapi
C 2	24.6	63.1	184748	2	AL160051 Homo sapi
C 3	24.2	62.1	67982	2	AC068869 Homo sapi
C 4	24.2	62.1	107839	2	AP000574 Homo sapi
C 5	24.2	62.1	114478	2	AP000489 Homo sapi
C 6	24.2	62.1	123500	2	AP000406 Homo sapi
C 7	24.2	62.1	128206	2	AP001258 Homo sapi
C 8	24.2	62.1	1225142	2	AP002358 Homo sapi
C 9	24.2	62.1	226020	2	AC087689 Homo sapi
C 10	24	61.5	195496	2	AL360214 Homo sapi
C 11	24	61.5	203257	9	AC013737 Homo sapi
C 12	23.8	61.0	1752	10	AF244362 Mus muscu
C 13	23.2	59.5	49743	2	AC017211 Drosophi
C 14	23.2	59.5	198721	2	AC010060 Drosophi
C 15	23.2	59.5	274585	3	AE003533 Drosophi
C 16	23	59.0	5767	10	DB3002 Mouse mR
C 17	23	59.0	12485	1	AE004962 Pseudom
C 18	23	59.0	68790	9	HSJ287H17 Human
C 19	23	59.0	136117	2	AC008700 Homo sapi
C 20	23	59.0	182127	2	AP001842 Homo sapi
C 21	23	59.0	184284	2	AC025582 Mus muscu
C 22	23	59.0	192110	2	AP004070 Oryza sat
C 23	23	59.0	226899	2	AL157832 Human
C 24	22.8	58.5	130192	9	AL157832 Human
C 25	22.8	58.5	157058	2	AL353725 Homo sapi
C 26	22.8	58.5	187344	9	AL354873 Human
C 27	22.6	57.9	174253	2	AC068590 Homo sapi
C 28	22.4	57.4	1148	9	MFNADIDGS Human
C 29	22.4	57.4	1285	9	HSJ69268 Human
C 30	22.4	57.4	1343	9	BC001902 Homo sapi
C 31	22.4	57.4	1362	9	BC000933 Homo sapi
C 32	22.4	57.4	1370	9	HSRMA1DH Human
C 33	22.4	57.4	1506	9	HSU40272 Human
C 34	22.4	57.4	18234	9	HSIDHTRAP Human
C 35	22.4	57.4	191923	9	AC087886 Homo sapi
C 36	22.4	57.4	230516	9	HSU52111 Homo sapi
C 37	22.2	56.9	13600	2	AC019859 Drosophi
C 38	22.2	56.9	151162	9	AC009364 Human
C 39	22.2	56.9	156508	3	AC007581 Drosophi
C 40	22.2	56.9	158648	2	AC021853 Homo sapi
C 41	22.2	56.9	170089	3	AC007925 Drosophi
C 42	22.2	56.9	188090	9	AC011625 Homo sapi
C 43	22.2	56.9	306848	3	AE003464 Drosophi
C 44	22	56.4	123386	8	FL2F1 Arabidops
C 45	22	56.4	134331	2	RM462P8 Rattus no

ALIGNMENTS

RESULT 1
AL354989/c
LOCUS
DEFINITION Homo sapiens chromosome 9 clone RP11-537H15, *** SEQUENCING IN
PROGRESS ***; 2 unordered pieces.
ACCESSION AL354989
VERSION AL354989.8 GI:15131225
KEYWORDS HTG; HTGS_PHRASE1; HTGS_ACTIVERFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
Direct Submission
Chapman, J.
1 (bases 1 to 178904)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CB10 15A, UK. E-mail enquiries: humquerry@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced g1.14715324.

COMMENT

Genome Center

```

Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba537H15
----- Summary Statistics
Sequencing vector: plasmid; version 4.5
Chemistry: Dye-terminator Big Dye, 100% of reads
Consensus quality: 177632 bases at least Q40
Consensus quality: 177660 bases at least Q30
Consensus quality: 177769 bases at least Q20
Insert size: 178804; sum-of-contigs
Insert size: 187738; 38.1% error; agarose-fp
Quality coverage: 16.40x in Q20 bases; sum-of-contigs Quality
coverage: 15.62x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*      1 176743: contig of 176743 bp in length
*      * 176744 176843: gap of 100 bp
*      * 176844 178904: contig of 2061 bp in length.
FEATURES
source
    location/Qualifiers
        1..178904
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="9"
            /clone="RP11-537A15"
            /clone_1fb="RPCI-11.2"
            /clone_lib="RPCI-11.2"
            /note="assembly_fragment:03560
fragment_chain:1
clone_end:17
vector_side:left"
misc_feature
    176844..178904
        /note="assembly_fragment:06048
fragment_chain:1"
BASE COUNT      52784 a 40958 c 39193 g 45869 t      100 others
ORIGIN
Query Match          63.1%; Score 24.6; DB 2; Length 178904;
Best Local Similarity 76.9%; Pred. No. 26;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0

Q      1 aggaagatggccttggtgaccttggaaatgcctctatt 39
      ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
Q      164878 AGGGGAGAGCCTTGTGACATAGATATGCGCTTGATT 164840

RESULT  2
LOCUS   AL160051/c                               HTG       27-JUN-2001
DEFINITION Homo sapiens chromosome 9 clone RP11-499G9, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
ACCESSION AL160051
VERSION   AL160051.15 GI:14575122
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   1 (Bases 1 to 184748)
TITLE     Plumb.B.
JOURNAL   Direct Submission
Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,

```

COMMENT

C310 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Jun 28, 2001 this sequence version replaced gi:14251856.

----- Genome Center

Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: BA49969
 ----- Summary Statistics

Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 179564 bases at least Q40
 Consensus quality: 180655 bases at least Q30
 Consensus quality: 181686 bases at least Q20
 Insert size: 183048; sum-of-contigs
 Insert size: 195118; 7.3% error; agarose-ff
 Quality coverage: 9.04x in Q20 bases; sum-of-contigs Quality coverage: 9.76x in Q20 bases; agarose-ff

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

*	1	13081:	contig of 13081 bp	in length
*	13082	13181:	gap of 100 bp	
*	13182	16296:	contig of 3115 bp	in length
*	16297	16396:	gap of 100 bp	
*	16397	57604:	contig of 41208 bp	in length
*	57605	57704:	gap of 100 bp	
*	57705	79988:	contig of 22284 bp	in length
*	79989	80088:	gap of 100 bp	
*	80089	95783:	contig of 15701 bp	in length
*	95790	95889:	gap of 100 bp	
*	95890	104909:	contig of 9020 bp	in length
*	104910	105009:	gap of 100 bp	
*	105010	117002:	contig of 11993 bp	in length
*	117003	117102:	gap of 100 bp	
*	117103	130858:	contig of 13756 bp	in length
*	130859	130958:	gap of 100 bp	
*	130959	140048:	contig of 9090 bp	in length
*	140049	140148:	gap of 100 bp	
*	140149	146397:	contig of 6249 bp	in length
*	146398	146497:	gap of 100 bp	
*	146498	148559:	contig of 2062 bp	in length
*	148560	148659:	gap of 100 bp	
*	148660	154236:	contig of 5577 bp	in length
*	154237	154336:	gap of 100 bp	
*	154337	156523:	contig of 2187 bp	in length
*	156524	156623:	gap of 100 bp	
*	156624	166567:	contig of 9944 bp	in length
*	166568	166667:	gap of 100 bp	
*	166668	173995:	contig of 7328 bp	in length
*	173996	174095:	gap of 100 bp	
*	174096	177017:	contig of 2922 bp	in length
*	177018	177117:	gap of 100 bp	
*	177118	181410:	contig of 4293 bp	in length
*	181411	181510:	gap of 100 bp	
*	181511	184748:	contig of 3208 bp	in length.

Location/Qualifiers

1..184748

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="9"
 /clone="RP11-499c9"
 /clone_1db="RPC1-11.2"
 misc_feature 1..13081

	/note="assembly_fragment:04097 fragment_chain:1"
misc_feature	13182..16296 /note="assembly_fragment:05055 fragment_chain:1"
misc_feature	16397..57604 /note="assembly_fragment:03961 fragment_chain:1" 57705..79988 /note="assembly_fragment:04593 fragment_chain:1"
misc_feature	80089..95789 /note="assembly_fragment:00809 fragment_chain:1" 95890..104909 /note="assembly_fragment:00531 fragment_chain:2"
misc_feature	105010..117002 /note="assembly_fragment:00210 fragment_chain:2" 117103..130858 /note="assembly_fragment:00996 fragment_chain:2"
misc_feature	130959..140048 /note="assembly_fragment:00505 fragment_chain:2" 140149..146397 /note="assembly_fragment:01143 fragment_chain:3"
misc_feature	146498..148559 /note="assembly_fragment:00279 fragment_chain:3" 148660..154236 /note="assembly_fragment:01326 fragment_chain:4"
misc_feature	154337..156523 /note="assembly_fragment:06423 fragment_chain:4" 156624..166567 /note="assembly_fragment:01495" 166668..173995 /note="assembly_fragment:02054" 174096..177017 /note="assembly_fragment:02923"
misc_feature	177118..181410 /note="assembly_fragment:03195" 181511..184748 /note="assembly_fragment:03511"
BASE COUNT	51200 a 42518 c 41831 g 47499 t 1700 others
ORIGIN	

	Query Match	63.1%;	Score 24.6;	DB 2;	Length 184748;	
	Best Local Similarity	76.9%;	Pred.No. 26;			
	Matches 30;	Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0
Oy	1 agagaaatgcgcttggtgccttggaaatgcgcttcatt 39					
Db	129317 AGGGGAAGGCCTTCTTGACATGAAATGCGCCTTGATT 129279					
RESULT	3					
LOCUS	AC068869/c					
DEFINITION	AC068869 67982 bp DNA HTG 10-MAY-2000					
ACCSSION	Homo sapiens chromosome 11 clone RP11-753E17 map 11, LOW-PASS SEQUENCE SAMPLING.					
VERSION	AC068869					
KEYWORDS	AC068869.1 GI:7767880					
SOURCE	HTG: HTGS_PHASE0.					
ORGANISM	human.					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS

REFERENCE	REFERENCE
AUTHORS	AUTHORS
TITLE	TITLE
JOURNAL	JOURNAL
REFERENCE	REFERENCE
AUTHORS	AUTHORS
(bases 1 to 67982)	
Brinen, B., Linton, L., Nusbaum, C. and Lander, E.	
Homio sapiens chromosome 11, clone RP11-753E17	
Unpublished	
2 (bases 1 to 67982)	
Anderson, S., Baldwin, J., Barna, N., Baster, E., V. Beda, F., Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Chioanello, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAngelis, K., Dewar, K., Diaz, J. S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Gelaian, J., Gargana, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, T., Johnson, R., Jones, C., Kam, L., Karatas, A., Klein, J., Larocque, K., Lamaras, R., Landers, T., Lehoczy, U., Levine, R., Lien, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McPheters, R., Meldrum, J., Meneses, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanis, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Traversan, M., Triglido, J., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.	
Direct Submission	
Submitted (10-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
All repeats were identified using RepeatMasker:	

```

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: I9390
Center clone name: 753_E_17
-----
** NOTE: This record contains 93 individual
** sequencing reads that have not been assembled into
** contigs. Runs of N are used to separate the reads
** and the order in which they appear is completely
** arbitrary. Low-pass sequence sampling is useful for
** identifying clones that may be gene-rich and allows
** overlap relationships among clones to be deduced.
** However, it should not be assumed that this clone
** will be sequenced to completion. In the event that
** the record is updated, the accession number will
** be preserved.
1
647 746: contig of 646 bp in length
747 746: gap of 100 bp
1364 1363: contig of 617 bp in length
1464 1463: gap of 100 bp
2073 2172: contig of 609 bp in length
2173 2806: contig of 634 bp in length
2807 2906: gap of 100 bp
2907 3536: contig of 630 bp in length
3537 3636: gap of 100 bp
3637 4233: contig of 597 bp in length
4234 4333: gap of 100 bp
4334 4970: contig of 637 bp in length
4971 5070: gap of 100 bp
5071 5668: contig of 598 bp in length
5669 5768: gap of 100 bp
5769 6382: contig of 614 bp in length
6383 6482: gap of 100 bp
6483 7124: contig of 642 bp in length
7125 7224: gap of 100 bp
7225 7858: contig of 634 bp in length

```

```

* 7859 7958: gap of 100 bp
* 7959 8603: contig of 645 bp in length
* 8604 8703: gap of 100 bp
* 8704 9350: contig of 647 bp in length
* 9351 9450: gap of 100 bp
* 9451 10065: contig of 615 bp in length
* 10066 10165: gap of 100 bp
* 10166 10797: contig of 632 bp in length
* 10798 10897: gap of 100 bp
* 10898 11522: contig of 625 bp in length
* 11523 11622: gap of 100 bp
* 11623 12251: contig of 629 bp in length
* 12252 12351: gap of 100 bp
* 12352 12988: contig of 637 bp in length
* 12989 13088: gap of 100 bp
* 13089 13708: contig of 620 bp in length
* 13709 13808: gap of 100 bp
* 13809 14453: contig of 645 bp in length
* 14454 14553: gap of 100 bp
* 14554 15193: contig of 640 bp in length
* 15194 15293: gap of 100 bp
* 15294 15925: contig of 632 bp in length
* 15926 16025: gap of 100 bp
* 16026 16640: contig of 615 bp in length
* 16641 16740: gap of 100 bp
* 16741 17378: contig of 638 bp in length
* 17379 17478: gap of 100 bp
* 17479 18084: contig of 606 bp in length
* 18085 18184: gap of 100 bp
* 18185 18825: contig of 641 bp in length
* 18826 18925: gap of 100 bp
* 18926 19545: contig of 620 bp in length
* 19546 19645: gap of 100 bp
* 19646 20303: contig of 658 bp in length
* 20304 20403: gap of 100 bp
* 20404 21035: contig of 637 bp in length
* 21036 21135: gap of 100 bp
* 21136 21796: contig of 661 bp in length
* 21797 21896: gap of 100 bp
* 21897 22533: contig of 637 bp in length
* 22534 22633: gap of 100 bp
* 22634 23256: contig of 623 bp in length
* 23257 23356: gap of 100 bp
* 23357 24007: contig of 651 bp in length
* 24008 24107: gap of 100 bp
* 24108 24751: contig of 644 bp in length
* 24752 24851: gap of 100 bp
* 24852 25480: contig of 629 bp in length
* 25481 25580: gap of 100 bp
* 25581 26192: contig of 612 bp in length
* 26193 26292: gap of 100 bp
* 26293 26899: contig of 607 bp in length
* 26900 26999: gap of 100 bp
* 27000 27609: contig of 610 bp in length
* 27610 27709: gap of 100 bp
* 27710 28333: contig of 624 bp in length
* 28334 28433: gap of 100 bp
* 28434 29067: contig of 634 bp in length
* 29068 29167: gap of 100 bp
* 29168 29822: contig of 655 bp in length
* 29823 29922: gap of 100 bp
* 29923 30589: contig of 667 bp in length
* 30590 30689: gap of 100 bp
* 30690 31333: contig of 644 bp in length
* 31334 31433: gap of 100 bp
* 31434 32076: contig of 643 bp in length
* 32077 32176: gap of 100 bp
* 32177 32817: contig of 641 bp in length
* 32818 32917: gap of 100 bp
* 32918 33544: contig of 627 bp in length
* 33545 33644: gap of 100 bp
* 33645 34293: contig of 649 bp in length
* 34294 34393: gap of 100 bp

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* 34394 35026: contig of 633 bp in length
* 35027 35125: gap of 100 bp
* 35127 35768: contig of 642 bp in length
* 35769 35868: gap of 100 bp
* 35869 36482: contig of 614 bp in length
* 36483 36582: gap of 100 bp
* 36583 37227: contig of 645 bp in length
* 37228 37327: gap of 100 bp
* 37328 37950: contig of 623 bp in length
* 37951 38050: gap of 100 bp
* 38051 38667: contig of 617 bp in length
* 38668 38767: gap of 100 bp
* 38768 39395: contig of 628 bp in length
* 39396 39495: gap of 100 bp
* 39496 40140: contig of 645 bp in length
* 40141 40240: gap of 100 bp
* 40241 40881: contig of 641 bp in length
* 40882 40981: gap of 100 bp
* 40982 41626: contig of 645 bp in length
* 41627 41726: gap of 100 bp
* 41727 42373: contig of 647 bp in length
* 42374 42473: gap of 100 bp
* 42474 43094: contig of 621 bp in length
* 43095 43194: gap of 100 bp
* 43195 43805: contig of 611 bp in length
* 43806 43905: gap of 100 bp
* 43906 44535: contig of 630 bp in length
* 44536 44635: gap of 100 bp
* 44636 45279: contig of 644 bp in length
* 45280 45379: gap of 100 bp
* 45380 46013: contig of 634 bp in length
* 46014 46113: gap of 100 bp
* 46114 46716: contig of 603 bp in length
* 46717 46816: gap of 100 bp
* 46817 47451: contig of 635 bp in length
* 47452 47551: gap of 100 bp
* 47552 48197: contig of 646 bp in length
* 48198 48297: gap of 100 bp
* 48298 48927: contig of 630 bp in length
* 48928 49027: gap of 100 bp
* 49028 49660: contig of 633 bp in length
* 49661 49760: gap of 100 bp
* 49761 50383: contig of 623 bp in length
* 50384 50483: gap of 100 bp

Query Match      62.1%; Score 24.2; DB 2; Length 67982;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY      1 agagatgccttgcttgctgaatgcctctta 37
Db 63244 AGTAGTGCGCAGTGTCTCTAGGAATGCGCTCTGA 63208

RESULT 4
AP000574/c
LOCUS      Homo sapiens chromosome 11 clone CMB9-49B9 map 11q12, WORKING DRAFT
DEFINITION
ACCESSION  AP000574.2 GI:8118782
VERSION    AP000574
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Homo sapiens DNA, clone: CMB9-49B9.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 107839)
REFERENCE  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
AUTHORS    Fujiyama,A., Yada,T., Totoki,Y., Matsubae,H. and Sakaki,Y.
TITLE      Homo sapiens 107,839 genomic DNA of 11q12
JOURNAL    Published Only in Database (1999) In press
REFERENCE  2 (bases 1 to 107839)
AUTHORS    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

```

TITLE
JOURNAL
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Submitted (08-OCT-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail: hattori@gsc.riken.go.jp,
URL: http://hnp.gsc.riken.go.jp/, Tel: 81-42-778-9923,
Fax: 81-42-778-9924)
On May 31, 2000 this sequence version replaced g1:6997466.

COMMENT

Center: RIKEN Genomic Sciences Center(GSC)

Center code: RIKEN

Web site: http://hnp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp

Project Information

Center project name: Humdraft11

Center clone name: CMB9-49B9

Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 101252 bases at least Q40

Consensus quality: 105065 bases at least Q30

Insert size: 107039; sum-of-contigs

Quality coverage: 4.56x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
9 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

```

1      24431 24330 contig of 24330 bp in length
      46451 46451 contig of 22021 bp in length
      46552 58483 contig of 11932 bp in length
      58584 69637 contig of 11054 bp in length
      69738 82347 contig of 12610 bp in length
      82448 91301 contig of 8854 bp in length
      91402 98707 contig of 7306 bp in length
      98808 105638 contig of 6831 bp in length
      105739 107839 contig of 2101 bp in length

Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1      24330: contig of 24330 bp in length
      24431 24430: gap of 100 bp
      24431 46451: contig of 22021 bp in length
      46452 46551: gap of 100 bp
      46552 58483: contig of 11932 bp in length
      58484 58583: gap of 100 bp
      58584 69637: contig of 11054 bp in length
      69638 69737: gap of 100 bp
      69738 82347: contig of 12610 bp in length
      82348 82447: gap of 100 bp
      82448 91301: contig of 8854 bp in length
      91302 91401: gap of 100 bp
      91402 98707: contig of 7306 bp in length
      98708 98807: gap of 100 bp
      98808 105638: contig of 6831 bp in length
      105639 105738: gap of 100 bp
      105739 107839: contig of 2101 bp in length.

Location/Qualifiers
1..107839
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

FEATURES

Source

```

misc_feature      /chromosome="11"
                  /map="11q12"
                  /clone="CMB9-49B9"
                  1..24330
                  /note="assembly_fragment clone_end.T7 vector_side:right"
misc_feature      24431..46451
                  /note="assembly_fragment"
misc_feature      46552..58483
                  /note="assembly_fragment"
misc_feature      58584..69637
                  /note="assembly_fragment"
misc_feature      69738..82347
                  /note="assembly_fragment"
misc_feature      82448..91301
                  /note="assembly_fragment"
misc_feature      91402..98707
                  /note="assembly_fragment"
misc_feature      98808..105638
                  /note="assembly_fragment"
misc_feature      105739..107839
                  /note="assembly_fragment"
BASE COUNT      30935 a 22634 c 22756 g 30714 t 800 others
ORIGIN

```

```

Query Match      62.1%; Score 24.2; DB 2; Length 107839;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 agagatggccttggtgcttggaatgctctta 37
Db 99866 AGRAGTGGCATGTTGCTAGGAATGGCTCTGA 99830

```

```

RESULT 5
AP000489/c      AP000489 114478 bp DNA HTG 30-MAY-2000
LOCUS          Homo sapiens chromosome 11 clone CMB9-7F5 map 11q13, WORKING DRAFT
DEFINITION
ACCESSION      AP000489.3 GI:8118775
VERSION        HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS       Homo sapiens DNA, clone: CMB9-7F5.
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                1 (bases 1 to 114478)
                Hattori, M., Yada, T., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
                Fujiyama, A., Ishii, K., Totoki, Y., Watanabe, H. and Sakaki, Y.
                Homo sapiens 114,478 genomic DNA of 11q13
                Published only in Database (1999) In press
                2 (bases 1 to 114478)
                Hattori, M., Yada, T., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
                Fujiyama, A., Ishii, K., Totoki, Y., Watanabe, H. and Sakaki, Y.
                Direct Submission
                Submitted (13-SEP-1999) Masahira Hattori, The Institute of Physical
                and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
                Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
                Japan (E-mail: hattori@gsc.riken.go.jp,
                URL: http://hnp.gsc.riken.go.jp/, Tel: 81-42-778-9923,
                Fax: 81-42-778-9924)
                On May 31, 2000 this sequence version replaced g1:6997459.
COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humdraft11
Center clone name: CMB9-7F5
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads

```

Assembly program: Phrap; version 0.990329
 Consensus quality: 109628 bases at least Q40
 Consensus quality: 112052 bases at least Q30
 Consensus quality: 113108 bases at least Q20
 Insert size: 113678; sum-of-ctrls
 Quality coverage: 6.65x in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 58724 contig of 58724 bp in length
 58825 83984 contig of 25160 bp in length
 84085 95379 contig of 11295 bp in length
 95480 105075 contig of 9596 bp in length
 105176 111400 contig of 6325 bp in length
 111501 113358 contig of 1838 bp in length
 113439 114478 contig of 1040 bp in length

Sequence updated (04-Nov-1999)
 Sequence updated (26-May-2000):

* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 58724: contig of 58724 bp in length
 58725 58824: gap of 100 bp
 58825 83984: contig of 25160 bp in length
 83985 84084: gap of 100 bp
 84085 95379: contig of 11295 bp in length
 95380 95479: gap of 100 bp
 95480 105075: contig of 9596 bp in length
 105076 105175: gap of 100 bp
 105176 111400: contig of 6225 bp in length
 111401 111500: gap of 100 bp
 111501 113358: contig of 1838 bp in length
 113359 113438: gap of 100 bp
 113439 114478: contig of 1040 bp in length.

FEATURES

SOURCE

1. 114478
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q13"
 /clone="CMB9-7F5"
 1. 58724
 /note="assembly-fragment"
 58825. 83984
 /note="assembly-fragment clone_end:17 vector_side:left"
 84085. 95379
 /note="assembly-fragment"
 95480. 105075
 /note="assembly-fragment"
 105176. 111400
 /note="assembly-fragment clone_end:SP6 vector_side:right"
 111501. 113358
 /note="assembly-fragment"
 113439. 114478
 /note="assembly-fragment"
 BASE COUNT 33314 a 23593 c 23225 g 33746 t 600 others
 ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 114478;
 Best Local Similarity 78.4%; Pred. No. 37;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agagatggccttggtgagccttgaatgacctcta 37
 Db 54667 AATGAGTGGCAATGTTCTTCAGGAATGGCTCTCGA 54631

RESULT 6
 AP000406/c
 LOCUS
 DEFINITION
 Homo sapiens chromosome 11 clone CMB9-21D9 map 11q12, WORKING DRAFT
 SEQUENCE, 4 unordered pieces.
 ACCESSION
 AP000406
 VERSION
 AP000406.4 GI:9927270
 KEYWORDS
 HTG; HTGS; PHASE1; HTGS; DRAFT.
 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens 123,300 genomic DNA of 11q12
 Published Only in Database (1999) In press
 2 (bases 1 to 123300)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 Submitted (27-AUG-1999) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-15-1 Kinasato, Sagamihara, Kanagawa 228-8555, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-42-778-9923, Fax:81-42-778-9924)
 On Aug 26, 2000 this sequence version replaced gi:8118745.

COMMENT

Center: RIKEN Genomic Sciences Center (GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 Project Information
 Center project name: HumDrafit1
 Center clone name: CMB9-21D9
 Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 121846 bases at least Q40
 Consensus quality: 122507 bases at least Q30
 Consensus quality: 122832 bases at least Q20
 Insert size: 123000; sum-of-ctrls
 Quality coverage: 13.07x in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 61533 contig of 61533 bp in length
 61634 106881 contig of 45248 bp in length
 106982 119565 contig of 12584 bp in length
 119666 123300 contig of 3635 bp in length.

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 61533: contig of 61533 bp in length
 61634 61633: gap of 100 bp
 61634 106881: contig of 45248 bp in length
 106882 106981: gap of 100 bp

JOURNAL
REFERENCE
AUTHORS
TITILE
JOURNAL
COMMENT

Published Only in Database (2000) In press
2 (bases 1 to 225142)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totokli,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jan 13, 2001 this sequence version replaced gi:8131622.

Sequencing vector:	PCR products	100% of reads
Chemistry:	Illumina	100% of reads
Sequencing:	Dye-terminator	EM-meshroom
Assembly program:	Pirapip	version 0.990329
Consensus quality:	219,945 bases	at least 940
Consensus quality:	22,218 bases	at least 930
Consensus quality:	22,348 bases	at least 920
Insert size:	223,342	sum-of-contigs
Quality coverage:	8.03x	sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 13 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

*	1	55748:	contig of	55748 bp	in length
*	55749	55848:	gap of	100 bp	
*	55849	81106:	contig of	25258 bp	in length
*	81107	81206:	gap of	100 bp	
*	81207	105043:	contig of	23837 bp	in length
*	105044	105143:	gap of	100 bp	
*	105144	129107:	contig of	23964 bp	in length
*	129108	129207:	gap of	100 bp	
*	129208	149114:	contig of	19907 bp	in length
*	149115	149214:	gap of	100 bp	
*	149215	165516:	contig of	16302 bp	in length
*	165517	165616:	gap of	100 bp	
*	165617	182204:	contig of	16588 bp	in length
*	182205	182304:	gap of	100 bp	
*	182305	192999:	contig of	10695 bp	in length
*	193000	193099:	gap of	100 bp	

```
misc_feature      1. .55748
                    /note="assembly-fragment clone_end:Spe vector_side:right
misc_feature      55849. .81106
                    /note="assembly-fragment"
misc_feature      81207. .105043
                    /note="assembly-fragment"
misc_feature      105144. .129107
                    /note="assembly-fragment"
misc_feature      129208. .149114
                    /note="assembly-fragment"
misc_feature      149215. .165516
                    /note="assembly-fragment"
misc_feature      165617. .182204
                    /note="assembly-fragment"
misc_feature      182305. .192999
                    /note="assembly-fragment"
misc_feature      193100. .203328
                    /note="assembly-fragment"
misc_feature      203429. .208865
                    /note="assembly-fragment clone_end:T7 vector_side:left"
misc_feature      208966. .216574
                    /note="assembly-fragment"
misc_feature      216675. .222800
                    /note="assembly-fragment"
misc_feature      222901. .225142
                    /note="assembly-fragment"
BASE COUNT      63054 a 46820 c 47221 g 66847 t 1200 others
ORIGIN
```

RESULT	9
AC087689	
LOCUS	
DEFINITION	Homo sapiens chromosome 11 clone RP11-103E20 map 11, WORKING DRAFT SEQUENCE, 9 unordered pieces.
ACCESSION	AC087689
VERSION	AC087689.3 GI:14210561
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (bases 1 to 226020)	Birren, B., Linton, L., Nusbaum, C. and Lander, E.	Homo sapiens chromosome II, clone RP11-1036E20	Unpublished	
2 (bases 1 to 226020)	Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.			

TITLE
JOURNAL
COMMENT

Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, P., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karates, A., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Margulis, N., Matthews, C., McCarthy, M., McKean, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Plunkhang, P., Pierre, N., Pollard, V., Raymond, C., Retta, R., Ribbeck, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Sudamanthan, A., Talamas, J., Testaye, S., Theodore, J., Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 27, 2001 this sequence version replaced g1:13123260.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L12345
Center clone name: 1036_E_20

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221473 bases at least Q40
Consensus quality: 222976 bases at least Q30
Consensus quality: 223564 bases at least Q20
Insert size: 224000; agarose-*fp*
Insert size: 225220; sum-of-*contigs*
Quality coverage: 8.7 in Q20 bases; agarose-*fp*
Quality coverage: 8.7 in Q20 bases; sum-of-*contigs*

NOTE: This is a 'working draft' sequence. It currently consists of 9 *contigs*. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the *contigs* are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2472: *contig* of 2472 bp in length
2473 2572: gap of 100 bp
2573 3289: *contig* of 717 bp in length
3290 3389: gap of 100 bp
3390 4086: *contig* of 697 bp in length
4087 4186: gap of 100 bp
4187 5709: *contig* of 1523 bp in length
5710 5809: gap of 100 bp
5810 17972: *contig* of 12163 bp in length
17973 18072: gap of 100 bp
18073 45215: *contig* of 27143 bp in length
45216 45315: gap of 100 bp
45316 92283: *contig* of 46968 bp in length
92284 92383: gap of 100 bp
92384 156424: *contig* of 64041 bp in length
156425 156524: gap of 100 bp
156525 226020: *contig* of 69496 bp in length.
Location/Qualifiers

source 1..226020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-1036E20"
/clone_lib="RP11-11 Human Male BAC"
1..2472
/note="assembly-fragment
clone_end:SP6
vector_side:left"
misc_feature 2573..3289
/note="assembly-fragment"
misc_feature 3390..4086
/note="assembly-fragment"
misc_feature 4187..5709
/note="assembly-fragment"
misc_feature 5810..17972
/note="assembly-fragment"
misc_feature 18073..45215
/note="assembly-fragment"
misc_feature 45316..92283
/note="assembly-fragment"
misc_feature 92384..156424
/note="assembly-fragment"
misc_feature 156525..226020
/note="assembly-fragment
clone_end:T7
vector_side:right"
BASE COUNT 66670 a 47794 c 46268 g 64486 t 802 others
ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 226020;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 1 aggaagtcgcttgatgcttgaatgctctta 37
Db 215819 AGTAGTGCGCAATGTTCCTAGGAATGCGCTCTGA 215855

RESULT 10
AL360214/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AL360214 195496 bp DNA HTG 04-AUG-2001
Homo sapiens chromosome 10 clone RP11-533N7, *** SEQUENCING IN PROGRESS ***
AL360214
AL360214.18 GI:15131258
HTG; HTGS_PHASE1; HTGS_ACTIVATED; HTGS_DRAFT; HTGS_FULLTOP.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 195496)
Chapman, J.
Direct Submission
Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced g1:15028671.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba533N7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 194004 bases at least Q40

FEATURES

ORIGIN	412	3	3	3	3
BASE COUNT	412	3	3	3	3

Query Match	Best Local Similarity	80.0%;	Score 23.8;	DB 10;	Length 1752;
Matches 28;	Conservative	0;	Mismatches	7;	Indels 0;
Gy	1	aggaaatgaccttgctgctgaaatgacgctct	35		
Db	972	AGGAGCTGGGCTTGCTGCTCGGAGAGGCCACT	938		

RESULT	13
LOCUS	AC017211/c
DEFINITION	Ac017211 49743 bp DNA HTG 09-DEC-1999
ACCESSION	AC017211
VERSION	AC017211.1 GI:6553775
KEYWORDS	HTG; HTGS_PHASE2.
SOURCE	fruit fly
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila. 1 (bases 1 to 49743) Adams,M. and Venter,J.C. Direct Submission Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA This sequence was identified as CDM:10209893 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES	source	Location/Qualifiers
		1. 49743
		/organism="Proscophila melanogaster"
		/db_xref="taxon:7227"
BASE COUNT	14017 a	10655 c 11128 g 13943 t
ORIGIN		
Query Match		59.5%; Score 23.2; DB 2; Length 49743;
Best Local Similarity		89.3%; Pred. No. 92;
Matches	25; Conservative	0; Mismatches 3; Indels 0; Gaps 0
QY	8 ggccttggtgacctggaatggccctt 35	
Db	40350 ggccttggtggccacgcgaatggccctt 40323	

RESULT	14
AC010060	
LOCUS	AC010060 198721 bp DNA HTG 29-MAY-2000
DEFINITION	Drosophila melanogaster clone RCP198-2ZJ22, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces.
ACCESSION	AC010060
VERSION	AC010060.8 GI:8101312
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SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 198721) Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K.,
AUTHORS	

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Lichterarge, O. Liu, J., Liu, W., Logan, O., Lozado, R. J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M. P., Mel, G., Morgan, M.,
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,
Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pi, L. L.,
Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sungang, R.,
Tabors, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M.,
Watlington, S., Weinstein, G., Weinstein, I. R., Williamson, A.,
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D., and
Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 198721)
Worley, K.C.
Submitted (11-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 29, 2000 this sequence version replaced gi:6996744.
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Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Project Information
Center project name: DBDO
Center clone name: RPC198-22J22
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Summary Statistics
Sequencing vector: M13: L088821
Chemistry: Dye-primer
Bodipy: 13% of reads
Chemistry: Dye-terminator
Big Dye: 44% of reads
Assembly program: Phrap; Version 0.960611
Consensus quality: 136940 bases at least Q40
Consensus quality: 159336 bases at least Q30
Consensus quality: 172208 bases at least Q20
Estimated insert size: 192862; sum-of-contigs estimation
Quality coverage: 2.8x in Q20 bases; sum-of-contigs estimation
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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5995: contig of 5995 bp in length
5996 6095: gap of unknown length
6096 11888: contig of 5793 bp in length
11889 11968: gap of unknown length
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18029 23565: contig of 5537 bp in length
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HTG.
SOURCE
fruit fly.
ORGANISM
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 274585)

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REFERENCE
AUTHORS
Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor
Miklos G.L., Abril J.F., Aghayani A., An H.J.,
Andrews Pfinckoch C., Baldwin D., Bailey R.M., Basu A.,
Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y.,
Benos P.V., Bertram B.P., Bhandari D., Bolshakov S., Borokova D.,
Botchan M.R., Bouck J., Brokstein P., Brotler P., Burris K.C.,
Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S.,

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